



results of BLAST

BLASTP 2.2.6 [Apr-09-2003]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1050528130-021341-18840

Query=

(533 letters)

Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF

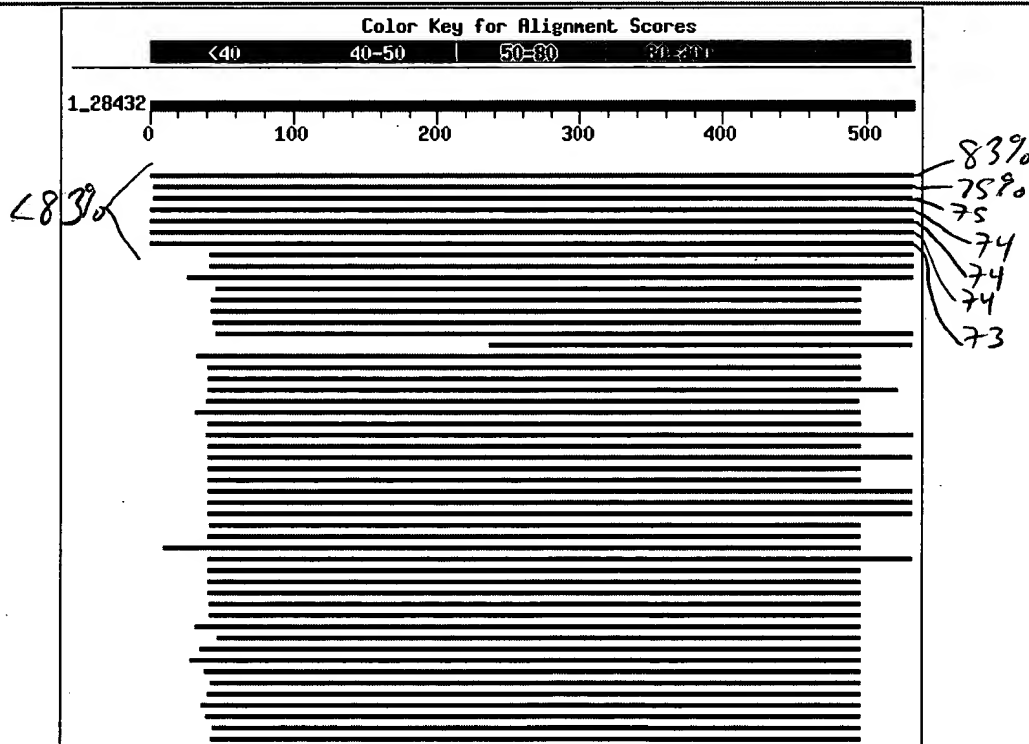
1,421,989 sequences; 457,202,972 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 110 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Score E

Sequences producing significant alignments:

(bits) Value

gi	5771354	dbj	BAA83501.1	Sucrose Transporter [Zea mays]	838	0.0
gi	9624451	gb	AAF90181.1	AF280050 1 sucrose transporter [Or...	758	0.0
gi	7489560	pir	T02982	probable sucrose transport protein -...	753	0.0
gi	20152871	gb	AAM13408.1	AF408842 1 sucrose transporter SU...	752	0.0
gi	7024415	emb	CAB75882.1	sucrose transporter 1 [Hordeum v...	751	0.0
gi	20152873	gb	AAM13409.1	AF408843 1 sucrose transporter SU...	749	0.0
gi	19548165	gb	AAL90455.1	AF408845 1 sucrose transporter SU...	747	0.0
gi	16152148	gb	AAL14982.1	AF419298 1 sucrose transporter [O...	586	e-166
gi	15718401	dbj	BAB68368.1	sucrose transporter [Oryza sati...	586	e-166
gi	21063927	gb	AAM29153.1	sucrose transporter 2 [Citrus si...	526	e-148
gi	29467454	dbj	BAC67164.1	sucrose transporter [Oryza sati...	526	e-148
gi	10119908	gb	AAG12987.1	AF166498 1 sucrose transporter-li...	525	e-148
gi	15227049	ref	NP 178389.1	putative sucrose/H+ symporter;...	523	e-147
gi	6434831	gb	AAF08330.1	AF021809 1 putative sucrose transp...	517	e-145
gi	29467456	dbj	BAC67165.1	sucrose transporter [Oryza sati...	502	e-141
gi	19071641	gb	AAL84308.1	AC073556 25 sucrose transporter, ...	416	e-115
gi	542020	pir	S43142	sucrose transport protein - castor be...	385	e-105
gi	4091891	gb	AAC99332.1	sucrose transporter [Apium graveo...	369	e-101
gi	15217601	ref	NP 177333.1	sucrose transport protein SUC1...	369	e-101
gi	5566434	gb	AAD45390.1	AF167415 1 sucrose transporter SUT...	367	e-100
gi	28172870	emb	CAD61275.1	sucrose transporter 4 protein [...	365	1e-99
gi	5882292	gb	AAD55269.1	AF182445 1 sucrose transporter [Vi...	364	2e-99
gi	15239949	ref	NP 196235.1	sucrose transporter protein; p...	364	2e-99
gi	1086253	pir	S38657	sucrose transport protein ptp1 - com...	364	2e-99
gi	18091779	gb	AAL58071.1	sucrose transporter SUC1 [Brassi...	364	2e-99
gi	5230818	gb	AAD41024.1	sucrose transport protein SUT1 [P...	363	4e-99
gi	15219938	ref	NP 173685.1	putative sucrose transport pro...	363	4e-99
gi	481131	pir	S38196	sucrose transport protein SUC2 - Arab...	363	4e-99
gi	7488866	pir	T12198	sucrose transport protein - fava bea...	363	5e-99
gi	7488936	pir	T14340	sucrose-proton transport protein - c...	363	6e-99
gi	7488935	pir	T14339	sucrose-proton transport protein - c...	362	6e-99
gi	6705993	dbj	BAA89458.1	sucrose transporter protein [Dau...	362	7e-99
gi	15219686	ref	NP 176830.1	sucrose-proton symporter, puta...	362	9e-99
gi	15217602	ref	NP 177334.1	putative sucrose transport pro...	362	1e-98
gi	12057172	emb	CAC19851.1	sucrose transporter [Arabidopsis...	361	1e-98
gi	20147213	gb	AAM10322.1	Atlg22710/T22J18_12 [Arabidopsis...	361	2e-98
gi	12038843	emb	CAC19689.1	sucrose/proton symporter [Daucu...	361	2e-98
gi	18091781	gb	AAL58072.1	sucrose transporter SUC2 [Brassi...	359	5e-98
gi	9957218	gb	AAG09270.1	AF176950 1 sucrose transporter [Ly...	359	6e-98
gi	10998390	gb	AAG25923.1	sucrose transporter SUT4 [Solanu...	358	9e-98
gi	6434829	gb	AAF08329.1	AF021808 1 putative sucrose transp...	358	2e-97
gi	9957053	gb	AAG09191.1	AF175321 1 sucrose transporter SUT...	356	6e-97
gi	15225986	ref	NP 179074.1	putative sucrose-proton sympor...	355	8e-97
gi	15218362	ref	NP 172467.1	putative sucrose/H+ symporter;...	355	1e-96
gi	542087	pir	JQ2389	sucrose transport protein - potato >g...	355	1e-96
gi	7649151	gb	AAF65765.1	AF242307 1 sucrose transport prote...	352	9e-96
gi	6434833	gb	AAF08331.1	AF021810 1 putative sucrose transp...	350	3e-95
gi	15239921	ref	NP 199174.1	sucrose transporter protein; p...	350	3e-95
gi	549000	sp	Q03411	STP SPIOL Sucrose transport protein (Su...	348	1e-94
gi	1076644	pir	S48789	sucrose transport protein - common t...	347	2e-94
gi	5823000	gb	AAD53000.1	U64967 1 sucrose-proton symporter ...	346	6e-94
gi	17447420	gb	AAF04295.2	AF191025 1 sucrose transporter 1 ...	345	8e-94
gi	6120115	gb	AAF04294.1	AF191024 1 sucrose transporter 1 [...	345	1e-93
gi	21063921	gb	AAM29150.1	citrus sucrose transporter 1 [Ci...	345	1e-93
gi	1086250	pir	S52377	sucrose transport protein SUC1 - com...	342	1e-92
gi	1076257	pir	S51114	sucrose-proton symporter - beet >gi ...	340	5e-92
gi	7024413	emb	CAB75881.1	sucrose transporter 2 [Hordeum v...	338	1e-91
gi	29467452	dbj	BAC67163.1	sucrose transporter [Oryza sati...	337	4e-91
gi	15217323	gb	AAK92667.1	AC090487 9 Putative sucrose trans...	318	2e-85
gi	25344709	pir	A86234	hypothetical protein [imported] - A...	315	1e-84
gi	575299	emb	CAA57726.1	sucrose transporter [Lycopersicon...	296	7e-79
gi	1076602	pir	S48788	sucrose transport protein - tomato (...	295	1e-78
gi	2980887	emb	CAA12256.1	Sucrose carrier [Ricinus communis]	295	1e-78



PubMed	Nucleotide	Protein	Genome	Structure	PMC	Taxonomy	MIM	Books	
Search		Protein	for					Go	Clear
		Limits	Preview/Index	History	Clipboard		Details		
Display	default	Show:	20	Send to	File	Get Subsequence			

☐ 1: BAA83501. Sucrose Transport...[gi:5771354]

[BLink](#), [Domains](#), [Links](#)

LOCUS BAA83501 521 aa linear PLN 26-AUG-1999
 DEFINITION Sucrose Transporter [Zea mays].
 ACCESSION BAA83501
 VERSION BAA83501.1 GI:5771354
 DBSOURCE accession [AB008464.1](#)
 KEYWORDS .

SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (sites)
 AUTHORS Aoki,N., Hirose,T., Takahashi,S., Ono,K., Ishimaru,K. and Ohsugi,R.
 TITLE Molecular cloning and expression analysis of a gene for a sucrose
 transporter in maize (Zea mays L.)

JOURNAL Plant Cell Physiol. (1999) In press

REFERENCE 2 (residues 1 to 521)

AUTHORS Aoki,N.
 TITLE Direct Submission
 JOURNAL Submitted (24-OCT-1997) Naohiro Aoki, Japan International Research
 Center for Agricultural Sciences, Biological Resources Division;
 1-2 Ohwashi, Tsukuba, Ibaraki 305, Japan
 (E-mail:naoki@ss.jircas.affrc.go.jp, Tel:81-0298-38-6305,
 Fax:81-0298-38-6650)

FEATURES Location/Qualifiers
 source 1..521
 /organism="Zea mays"
 /db_xref="taxon:4577"
 Protein 1..521
 /product="Sucrose Transporter"
 CDS 1..521
 /gene="ZmSUT1"
 /coded_by="AB008464.1:168..1733"

ORIGIN

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61 yvqtlglsha ltsfmwlcgp iaglvvqplv glysdrcstar wgrrrpfili gcmliclavi
121 vvgfssdiga algdtkehcs lyhgprwhaa ivyvlgfll dfsnntvqgp arammadlcg
181 hhgpsaansi fcswmalgni lgyssgstnn whkwfpfllt nacceacanl kgaflvavvf
241 lvmcltvtlf fanevpyrgn qnlptkange vetepsgpla vlkgfknlp gmpsvllvtg
301 ltwlswfpfi lydtldwmgre iyhgdpkgsn aqisafdegv rvgsfgllln sivlgfssfl
361 iepmcrkvqp rvvwtsnfm vcvamaatal isfwsldkyh gyvqdaitas tsikavclvl
421 faflgvplai lysvpfavta qlaatkgggq glctgvlnis ivipqviial gagpwdalfg
481 kgnipafgva sgfaliggvv gvfillpkisk rqfravsagg h

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gi	4960089	gb	AAD34610.1	AF149981.1	sucrose transporter-lik...	294	2e-78	
gi	16930709	gb	AAL32020.1		sucrose transporter [Vitis vinif...	277	2e-73	
gi	13186184	emb	CAC33492.1		sucrose carrier [Ricinus communis]	269	8e-71	
gi	14161680	gb	AAK54856.1		sucrose transporter [Oryza sativa]	241	2e-62	
gi	14161682	gb	AAK54857.1		sucrose transporter [Oryza sativa]	239	6e-62	
gi	27227722	emb	CAD29832.1		sucrose transporter [Viscum alb...	222	1e-56	
gi	17402525	dbj	BAB78696.1		sucrose transporter [Nicotiana ...]	220	4e-56	
gi	28830172	gb	AAO52628.1		similar to Arabidopsis thaliana ...	211	3e-53	
gi	5640023	gb	AAD45932.1	AF168771.1	sucrose transport prote...	211	3e-53	
gi	28371870	gb	AAO38059.1		sucrose transporter SUC1 [Brassi...	177	3e-43	
gi	28143940	gb	AAO26335.1		putative sucrose transporter [Br...	159	2e-37	
gi	27447671	gb	AAO13696.1		sucrose transporter [Lycopersico...	137	4e-31	
gi	26522780	dbj	BAC44864.1		hypothetical protein [Glycine max]	110	5e-23	
gi	11596257	gb	AAG38546.1	AF309805.1	putative sucrose carr...	102	2e-20	
gi	28917846	gb	EAA27533.1		hypothetical protein [Neurospora...	100	7e-20	
gi	19115299	ref	NP_594387.1		putative sucrose carrier [Schi...	99	1e-19	
gi	21426811	ref	NP_653348.1		proton-associated sugar transp...	99	2e-19	L
gi	16716355	ref	NP_444307.1		membrane associated transporte...	98	3e-19	L
gi	21293355	gb	EAA05500.1		agCP10413 [Anopheles gambiae str...	98	4e-19	
gi	17369709	sp	Q9UMX9	MATP HUMAN	Membrane-associated transp...	97	5e-19	L
gi	26354753	dbj	BAC41003.1		unnamed protein product [Mus mu...	97	5e-19	L
gi	28872809	ref	NP_057264.2		membrane-associated transporte...	97	5e-19	L
gi	15004313	gb	AAK77024.1	AF332510.1	membrane-associated tr...	97	6e-19	
gi	27688281	ref	XP_226834.1		similar to membrane associated...	97	7e-19	L
gi	27719225	ref	XP_235397.1		similar to KIAA1126 protein [H...	95	3e-18	L
gi	13097810	gb	AAH03597.1	AAH03597	Similar to AIM-1 protein...	92	2e-17	L
gi	27948583	gb	AAO25647.1		membrane-associated transporter ...	92	2e-17	
gi	21244213	ref	NP_643795.1		sugar transporter [Xanthomonas...	92	2e-17	
gi	24661424	ref	NP_648292.1		CG4484-PA [Drosophila melanoga...	91	4e-17	L
gi	21232786	ref	NP_638703.1		sugar transporter [Xanthomonas...	89	1e-16	
gi	6651341	gb	AAF22281.1	AF167417.1	putative sucrose transp...	88	4e-16	
gi	22122421	ref	NP_666089.1		hypothetical protein MGC32471 ...	85	3e-15	L
gi	27712020	ref	XP_222629.1		similar to hypothetical protei...	84	4e-15	L
gi	14916437	ref	NP_149093.1		prostein protein [Homo sapiens...	83	1e-14	L
gi	21294249	gb	EAA06394.1		ebiP8133 [Anopheles gambiae str....]	81	3e-14	
gi	13874497	dbj	BAB46871.1		hypothetical protein [Macaca fa...	81	4e-14	
gi	6473156	dbj	BAA87101.1		Hypothetical protein [Schizosacc...	79	1e-13	

Alignments

Get selected sequences

Select all

Deselect all

☐ >gi|5771354|dbj|BAA83501.1| Sucrose Transporter [Zea mays]

Length = 521

Score = 838 bits (2166), Expect = 0.0

Identities = 447/538 (83%), Positives = 461/538 (85%), Gaps = 22/538 (4%)

Query: 1 MARGDGGQLAELSAGVRGAAA-----VVDHVAPISLGRILLAGMVAPISLGRILLAGMVA 55
MARGDG ELS GVRG DHVAPISLG RLILLAGMVA

Sbjct: 1 MARGDGE--LELSVGVRGTGGAAAAAADHVAPISLG-----RLILLAGMVA 44

Query: 56 GGVQYGWALQLSLLTPYVQTLGLSHALTSFMWLCPGPIAGLVVQPLVGLYSDRCTSRWGRR 115
GGVQYGWALQLSLLTPYVQTLGLSHALTSFMWLCPGPIAGLVVQPLVGLYSDRCT+RWGRR

Sbjct: 45 GGVQYGWALQLSLLTPYVQTLGLSHALTSFMWLCPGPIAGLVVQPLVGLYSDRCTARWGRR 104

Query: 116 RPFILTGCMCLICVAVIVVGFSSDIGAALGDTKEHCSTLYHGPRWHAAIVYVLGFWLLDFSN 175
RPFIL GCMLIC+AVIVVGFSSDIGAALGDTKEHCSTLYHGPRWHAAIVYVLGFWLLDFSN

Sbjct: 105 RPFILIGCMCLICVAVIVVGFSSDIGAALGDTKEHCSTLYHGPRWHAAIVYVLGFWLLDFSN 164

Query: 176 NTVQGPARAMMADLCDHHGPSAANSIFCSWMALGNILGYSSGSTNNWHKWFPLKTSACC 235

NTVQGPARAMMADLC HHGPSAANSIFCSWMALGNILGYSSGSTNNWHKWFPFL T+ACC
 Sbjct: 165 NTVQGPARAMMADLCGHHGPSAANSIFCSWMALGNILGYSSGSTNNWHKWFPFLTNACC 224

Query: 236 EACANLKGXXXXXXXXXXXXXXXXXXXXXIFAKEVPYRANENLPTTKAGGEVETEPTGPLAVLK 295
 EACANLKG FA EVPYR N+NLP TKA GEVETEP+GPLAVLK
 Sbjct: 225 EACANLKGAFVLAVVFLVMCLTTLFFANEVPGRNQNLN- TKANGEVETEPSGPLAVLK 283

Query: 296 GFKDLPPGMPVSVLLVTAITWLSWFPFILIYD TDWMDGREIYHGD PKGSNAQISAFNEGV RVG 355
 GFK+LP GMPVSVLLVT +TWLSWFPFILIYD TDWMDGREIYHGD PKGSNAQISAF+EGV RVG
 Sbjct: 284 GFKNLPTGMPVSVLLVTGLTWLSWFPFILIYD TDWMDGREIYHGD PKGSNAQISAFDEGV RVG 343

Query: 356 AFGLLLNSVILGFSSFLIEPMCRKVGPRVWVTSNFMVCVAMAATALISFWSLRDYG YV 415
 +FGLLLS++LGFSSFLIEPMCRKVGPRVWVTSNFMVCVAMAATALISFWSL+DYG YV
 Sbjct: 344 SFGLLLNSIVLGFSSFLIEPMCRKVGPRVWVTSNFMVCVAMAATALISFWSLKDYHGYV 403

Query: 416 QDAITANASIKAVCLVLF AFLGVPLAILYSVPFAVTAQLAATRGGGQGLCTGVLNISIVI 475
 QDAITA+ SIKAVCLVLF AFLGVPLAILYSVPFAVTAQLAAT+GGGQGLCTGVLNISIVI
 Sbjct: 404 QDAITASTSIKAVCLVLF AFLGVPLAILYSVPFAVTAQLAATKGGGQGLCTGVLNISIVI 463

Query: 476 PQVIALGAGPWDALFGKGNIPXXXXXXXXXXXXXXXXXXXXXPKISKRQFRAVSAGGH 533
 PQVIALGAGPWDALFGKGNIP PKISKRQFRAVSAGGH
 Sbjct: 464 PQVIALGAGPWDALFGKGNIPAFGVASGFALIGGVGVFLLPKISKRQFRAVSAGGH 521

☐ >gi|9624451|gb|AAF90181.1|AF280050 1 sucrose transporter [Oryza sativa (indica c
 Length = 538

Score = 758 bits (1958), Expect = 0.0

Identities = 399/529 (75%), Positives = 432/529 (81%), Gaps = 4/529 (0%)

Query: 4 GDGGQLAELSAGVRGAAAVVDHVAPISLGRILLAGMVAPISLGRILLAGMVAGGVQYGWA 63
 G GG ELS G APISLGRILLAGMVAGGVQYGWA
 Sbjct: 12 GGGGGGLELS---VGVGGGGGARGGGGGEAAAAVETAAPISLGRILLAGMVAGGVQYGWA 68

Query: 64 LQLSLLTPYVQTLGLSHALTSFMWLCGPIAGLVVQPLVGLYSDRCTSRWGRRRPFILTGC 123
 LQLSLLTPYVQTLGLSHALTSFMWLCGPIAG+VVQP VGLYSDRCTS+WGRRRP+ILTGC
 Sbjct: 69 LQLSLLTPYVQTLGLSHALTSFMWLCGPIAGMVVQPCVGLYSDRCTSKWGRRRPPYILTGC 128

Query: 124 MLICVAVIVVGFSSDIGAALGDTKEHCSLYHGPRWHAAIVYVLGFWLLDFSNNTVQGP AR 183
 +LIC+AV+V+GFS+DIG A+GDTKE CS+YHG RWHAAIVYVLGFWLLDFSNNTVQGP AR
 Sbjct: 129 VLICLAVVIGFSADIGYAMGDTKEDCSVYHGSRWHAAIVYVLGFWLLDFSNNTVQGP AR 188

Query: 184 AMMADLCDHHGPSAANSIFCSWMALGNILGYSSGSTNNWHKWFPFLKTSACCEACANLKG 243
 A+MADL HGP ANSIFCSWMA+GNILGYSSGSTNNWHKWFPFLKT ACCEACANLKG
 Sbjct: 189 ALMADLSGRHGP GTANSIFCSWMAMGNILGYSSGSTNNWHKWFPFLKTRACCEACANLKG 248

Query: 244 XXXXXXXXXXXXXXXXXXXXIFAKEVPYRANENLPTTKAGGEVETEPTGPLAVLKGFKDLP PG 303
 IFAKEVP++ N LP TK+ E E TGPLAVLKGF++LP G
 Sbjct: 249 AFLVAVIFLSLCLVITLIFAKEVPFKGNAALP-TKSNEPAEPEGTGPLAVLKGFRLNLP TG 307

Query: 304 MPSVLLVTAITWLSWFPFILIYD TDWMDGREIYHGD PKGSNAQISAFNEGV RVGAFGLLLNS 363
 MPSVL+VT +TWLSWFPFILIYD TDWMDGREIYHGD PKG++ QI AFN+GVR GAFGLLLNS
 Sbjct: 308 MPSVLIVTGLTWLSWFPFILIYD TDWMDGREIYHGD PKGTD PQIEAFNQGV RAGAFGLLLNS 367

Query: 364 VILGFSSFLIEPMCRKVGPRVWVTSNFMVCVAMAATALISFWSLRDYG YVQDAITANA 423
 ++LGFSSFLIEPMCRKVGPRVWVTSNFMVCVAMAATALISFWSL+D+HG VQ AITA+
 Sbjct: 368 IVLGFSSFLIEPMCRKVGPRVWVTSNFMVCVAMAATALISFWSLKD FHTVQKAITADK 427

Query: 424 SIKAVCLVLF AFLGVPLAILYSVPFAVTAQLAATRGGGQGLCTGVLNISIVIPQVIALG 483
 SIKAVCLVLF AFLGVPLA+LYSVPF AVTAQLAATRGGGQGLCTGVLNISIVIPQV+IALG
 Sbjct: 428 SIKAVCLVLF AFLGVPLAVLYSVPF AVTAQLAATRGGGQGLCTGVLNISIVIPQVVIALG 487

Query: 484 AGPWDALFGKGNIPXXXXXXXXXXXXXXXXXXXXXPKISKRQFRAVSAGG 532
 AGPWD LFGKGNIP PKISKRQFR+VS GG
 Sbjct: 488 AGPWDELFGKGNIPAFGLASGFALIGGVAGIFLLPKISKRQFRSVSMGG 536

☐ >gi|7489560|pir|T02982 probable sucrose transport protein - rice
gi|2723471|dbj|BAA24071.1| sucrose transporter [Oryza sativa (japonica cultivar-g
Length = 537

Score = 753 bits (1944), Expect = 0.0

Identities = 397/529 (75%), Positives = 430/529 (81%), Gaps = 5/529 (0%)

Query: 4 GDGGQLAELSAGVRGAAAVVDHVAPISLGRILLAGMVAPISLGRILLAGMVAGGVQYGWA 63
G GG ELS APISLGRILLAGMVAGGVQYGWA
Sbjct: 12 GGGGGGLELS----VGVGGGGARGGGGGEAAAETAAPISLGRILLAGMVAGGVQYGWA 67

Query: 64 LQLSLLTPYVQTLGLSHALTSFMWLCGPIAGLVVQPLVGLYSDRCTSRWGRRRPFILTC 123
LQLSLLTPYVQTLGLSHALTSFMWLCGPIAG+VVQP VGLYSDRCTS+WGRRRP+ILTC
Sbjct: 68 LQLSLLTPYVQTLGLSHALTSFMWLCGPIAGMVVQPCVGLYSDRCTSKWGRRRPYILTC 127

Query: 124 MLICVAVIVVGFSSDIGAALGDTKEHCSLYHGPRWHAAIVYVLGFLLDFSNNTVQGP 183
+LIC+AV+V+GFS+DIG A+GDTKE CS+YHG RWHAIVYVLGFLLDFSNNTVQGP
Sbjct: 128 VLICLAVVIGFSADIGYAMGDTKEDCSVYHGSRWHAAIVYVLGFLLDFSNNTVQGP 187

Query: 184 AMMADLCDHHGPSAANSIFCSWMALGNILGYSSGSTNNWHKWFPFLKTSACCEACANLKG 243
A+MADL HGP ANSIFCSWMA+GNILGYSSGSTNNWHKWFPFLKT ACCEACANLKG
Sbjct: 188 ALMADLSGRHGPGTANSIFCSWMAMGNILGYSSGSTNNWHKWFPFLKTRACCEACANLKG 247

Query: 244 XXXXXXXXXXXXXXXXXXXXIFAKEVPYRANENLPTTKAGGEVETEPTGPLAVLKGFCDLPPG 303
IFAKEVP++ N LP TK+ E E TGPLAVLKGF++LP G
Sbjct: 248 AFLVAVIFLSLCLVITLIFAKEVPFKGNAALP-TKSNEPAEPEGTGPLAVLKGFRLNPTG 306

Query: 304 MPSVLLVTAITWLSWFPFILIYDTDWMGREIYHGDPKGSNAQISAFNEGVRVGAFLGLLNS 363
MPSVL+VT +TWLSWFPFILIYDTDWMGREIYHGDPKG++ QI AFN+GVR GAFGLLNS
Sbjct: 307 MPSVLIVTGLTWLSWFPFILIYDTDWMGREIYHGDPKGTDPQIEAFNQVRAGAFGLLNS 366

Query: 364 VILGFSSFLIEPMCRKVGPRVWVTSNFMVCVAMAATALISFWSLRDYHGYVQDAITANA 423
++LGFSSFLIEPMCRKVGPRVWVTSNF+VC+AMAATALISFWSL+D+HG VQ AITA+
Sbjct: 367 IVLGFSSFLIEPMCRKVGPRVWVTSNFLVCIAAMAATALISFWSLKDFHGTQKAITADK 426

Query: 424 SIKAVCLVLF AFLGVPLAILYSVPFAVTAQLAATRGGGQGLCTGVLNISIVIPQVIALG 483
SIKAVCLVLF AFLGVPLA+LYSVPFAVTAQLAATRGGGQGLCTGVLNISIVIPQV+IALG
Sbjct: 427 SIKAVCLVLF AFLGVPLAVLYSVPFAVTAQLAATRGGGQGLCTGVLNISIVIPQVVIALG 486

Query: 484 AGPWDALFGKGNIPXXXXXXXXXXXXXXXXXXXXXPKISKRQFRAVSAGG 532
AGPWD LFGKNIP PKISKRQF +VS GG
Sbjct: 487 AGPWDELFGKGNIPAFGLASGFALIGGVAGIFLLPKISKRQFWSVSMGG 535

☐ >gi|20152871|gb|AAM13408.1|AF408842.1 sucrose transporter SUT1A [Triticum aestiv
Length = 522

Score = 752 bits (1941), Expect = 0.0

Identities = 398/533 (74%), Positives = 435/533 (81%), Gaps = 11/533 (2%)

Query: 1 MARGDGGQLAELSAGVRGAAAVVDHVAPISLGRILLAGMVAPISLGRILLAGMVAGGVQY 60
MARG G ELS GV G A ++ ISLGRILLAGMVAGGVQY
Sbjct: 1 MARGGGNGEVELSVGVGGGGAGAGGADAPAVD-----ISLGRILLAGMVAGGVQY 50

Query: 61 GWALQLSLLTPYVQTLGLSHALTSFMWLCGPIAGLVVQPLVGLYSDRCTSRWGRRRPFIL 120
GWALQLSLLTPYVQTLGLSHALTSFMWLCGPIAGLVVQP VGLYSD+CTSRWGRRRPFIL
Sbjct: 51 GWALQLSLLTPYVQTLGLSHALTSFMWLCGPIAGLVVQPCVGLYSDKCTSRWGRRRPFIL 110

Query: 121 TGCMLICVAVIVVGFSSDIGAALGDTKEHCSLYHGPRWHAAIVYVLGFLLDFSNNTVQG 180
TGC+LIC+AV+VVGFS+DIGAALGD+KE CSLYHGPRWHAAIVYVLGFLLDFSNNTVQG
Sbjct: 111 TGCILICIAVVVGFSAIDIGAALGDSKEECSLYHGPRWHAAIVYVLGFLLDFSNNTVQG 170

Query: 181 PARAMMADLCDHHGPSAANSIFCSWMALGNILGYSSGSTNNWHKWFPFLKTSACCEACAN 240
PARA+MADL HGPSAANSIFCSWMALGNILGYSSGSTNNWHKWFPFL+T ACCEACAN
Sbjct: 171 PARALMADLSAQHGPSAANSIFCSWMALGNILGYSSGSTNNWHKWFPFLRTRACCEACAN 230

Query: 241 LKGXXXXXXXXXXXXXXXXXXXXIFAKEVPYRANENLPTTKAGGEVETEPTGPLAVLKGFKDL 300
 LKG IFAKE+PY+A LP TKA G+VE EPTGPLAV KGFK+L
 Sbjct: 231 LKGAFVLAVLFLAFCLVITVIFAKEIPYKAIAPLP-TKANGQVEVEPTGPLAVFKGFKNL 289

Query: 301 PPGMPSVLLVTAITWLSWFPFILIYDTDWMGREIYHGD PKGSNAQISAFNEGVRVGA FGLL 360
 PPGMPSVLLVT +TWLSWFPFILIYDTDWMGREIYHGD PKG+ + +AF GVR GAFGLL
 Sbjct: 290 PPGMPSVLLVTGLTWLSWFPFILIYDTDWMGREIYHGD PKGTPDEANAFQAGVRAGAFGLL 349

Query: 361 LNSVILGFSSFLIEPMC RKVGPRVWVTSNFMVCVAMAATALISFWSLRDYG YVQDAIT 420
 LNSV+LGFSSFLIEP+C+++GPRVWV+SNF+VC++MAA +IS+W+ +D HGY+Q AIT
 Sbjct: 350 LNSVILGFSSFLIEPLCKRLGPRVWVSSN FLVCLSM A AICIISWWATQDLHG YIQHAIT 409

Query: 421 ANASIKAVCLVLFAFLGVPLAILYSVPFAVTAQLAATRGGGQGLCTGVLNISIVIPQVII 480
 A+ IK V L LFAFLG+PLAILYSVPFAVTAQLAA RGGGQGLCTGVLNI+IVIPQVII
 Sbjct: 410 ASKEIKIVSLALFAFLGIPLAILYSVPFAVTAQLAANRGGGQGLCTGVLNIAIVIPQVII 469

Query: 481 ALGAGPWDALFGKGNIPXXXXXXXXXXXXXXXXXXXXPKISKRQFRAVSAGGH 533
 A+GAGPWD LFGKGNIP PKIS+RQFRAVS GGH
 Sbjct: 470 AVGAGPWDELFGKGNIPAFGVASAFALIGGIVGIFLLPKISRRQFRAVSGGGH 522

☐ >gi|7024415|emb|CAB75882.1| sucrose transporter 1 [Hordeum vulgare subsp. vulgar]
 Length = 523

Score = 751 bits (1939), Expect = 0.0
 Identities = 399/538 (74%), Positives = 434/538 (80%), Gaps = 20/538 (3%)

Query: 1 MARGDGGQLAELS-----AGVRGAAAVVDHVAPISLGR LILAGMVAPISLGR LILAGMVA 55
 MARG G ELS G A + ISLG RLILAGMVA
 Sbjct: 1 MARGGGNGEVELSVGVGGGGGGAAPRAEPAVQISLG-----RLILAGMVA 46

Query: 56 GGVQYGWALQLSLLTPYVQTLGLSHALTSFMWLCGPIAGLVVQPLVGLYSDRCTSRWGRR 115
 GGVQYGWALQLSLLTPYVQTLGLSHALTSFMWLCGPIAGLVVQP VGLYSD+CTSRWGRR
 Sbjct: 47 GGVQYGWALQLSLLTPYVQTLGLSHALTSFMWLCGPIAGLVVQPCVGLYSDKCTSRWGRR 106

Query: 116 RPFILTGCM LICVAVIVVGFSSDIGAALGDTKEHCSLYHGPRWHAAIVYVLGFWLLDFSN 175
 RPFILTG C+LIC+AVI+VGFS+DIGAALGD+KE CSLYHGPRWHAAIVYVLGFWLLDFSN
 Sbjct: 107 RPFILTGCVLICLA V IIVGFSADIGAALGDSKEECSLYHGPRWHAAIVYVLGFWLLDFSN 166

Query: 176 NTVQGPARAMMADLCDHHGPSAANSIFCSWMALGNILGYSSGSTNNWHKWFPFLKTSACC 235
 NTVQGPARA+MADL HGPSAANSIFCSWMALGNILGYSSGSTNNWHKWFPFL+T ACC
 Sbjct: 167 NTVQGPARAMADLSAQHGPSAANSIFCSWMALGNILGYSSGSTNNWHKWFPFLRTRACC 226

Query: 236 EACANLKGXXXXXXXXXXXXXXXXXXXXIFAKEVPYRANENLPTTKAGGEVETEPTGPLAVLK 295
 EACANLKG IFAKEVPY+A LP TKA G+VE EPTGPLAV K
 Sbjct: 227 EACANLKGAFVLAVLFLSLALVITLIFAKEVPYKAIAPLP-TKANGQVEVEPTGPLAVFK 285

Query: 296 GFKDLPPGMPSVLLVTAITWLSWFPFILIYDTDWMGREIYHGD PKGSNAQISAFNEGVRVG 355
 GFK+LPPGMPSVLLVT +TWLSWFPFILIYDTDWMGREIYHGD PKG+ A+ +AF EGVR G
 Sbjct: 286 GFKNLPPGMPSVLLVTGLTWLSWFPFILIYDTDWMGREIYHGD PKGTPAEANAFQEGVRAG 345

Query: 356 AFGLLLN SVILGFSSFLIEPMC RKVGPRVWVTSNFMVCVAMAATALISFWSLRDYG YV 415
 AFGLLLN SV+LGFSSFLIEPMC+++GPRVWV+SN +VC++MAA +IS+W+ +D HGY+
 Sbjct: 346 AFGLLLN SVILGFSSFLIEPMCRLGPRVWVSSNMLVCLSM A AICIISWWATQDLHG YI 405

Query: 416 QDAITANASIKAVCLVLFAFLGVPLAILYSVPFAVTAQLAATRGGGQGLCTGVLNISIVI 475
 Q AITA+ IKAV L LFAFLG+PLAILYSVPFAVTAQLAA +GGGQGLCTGVLNI+IVI
 Sbjct: 406 QHAITASKEIKAVSLALFAFLGIPLAILYSVPFAVTAQLAANKGGGQGLCTGVLNIAIVI 465

Query: 476 PQVIIALGAGPWDALFGKGNIPXXXXXXXXXXXXXXXXXXXXPKISKRQFRAVSAGGH 533
 PQVIIA+GAGPWD LFGKGNIP PKIS+RQFRAVS GGH
 Sbjct: 466 PQVIIAVGAGPWDELFGKGNIPAFGMASVFALIGGVVIGIFLLPKISRRQFRAVSGGGH 523

☐ >gi|20152873|gb|AAM13409.1|AF408843.1 sucrose transporter SUT1B [Triticum aestiv]
 Length = 522

Score = 749 bits (1934), Expect = 0.0

Identities = 398/533 (74%), Positives = 434/533 (81%), Gaps = 11/533 (2%)

Query: 1 MARGDGGQLAELSAGVRGAAAVVDHVAPISLGRILLAGMVAPISLGRILLAGMVAGGVQY 60
 MARG G ELS GV G A ++ ISLGRILLAGMVAGGVQY
 Sbjct: 1 MARGGGNGEVELSVGVGGGGAGAGGADAPAVD-----ISLGRILLAGMVAGGVQY 50

Query: 61 GWALQLSLLTPYVQTLGLSHALTSFMWLCGPIAGLVVQPLVGLYSDRCTSRWGRRRPFIL 120
 GWALQLSLLTPYVQTLGLSHALTSFMWLCGPIAGLVVQP VGLYSD+CTSRWGRRRPFIL
 Sbjct: 51 GWALQLSLLTPYVQTLGLSHALTSFMWLCGPIAGLVVQPCVGLYSDKCTSRWGRRRPFIL 110

Query: 121 TGCMLICVAVIVVGFSSDIGAALGDTKEHCSLYHGPRWHAAIVYVLGFWLLDFSNNTVQG 180
 TG +LIC+AV+VVGFS+DIGAALGD+KE CSLYHGPRWHAAIVYVLGFWLLDFSNNTVQG
 Sbjct: 111 TGYILICIAVVVVGFSADIGAALGDSKEECSLYHGPRWHAAIVYVLGFWLLDFSNNTVQG 170

Query: 181 PARAMMADLCDHHGPSAANSIFCSWMALGNILGYSSGSTNNWHKWFPFLKTSACCEACAN 240
 PARA+MADL HGPSAANSIFCSWMALGNILGYSSGSTNNWHKWFPFL+T ACCEACAN
 Sbjct: 171 PARALMADLSAQHGPSAANSIFCSWMALGNILGYSSGSTNNWHKWFPFLRTRACCEACAN 230

Query: 241 LKGXXXXXXXXXXXXXXXXXXXXXIFAKEVPYRANENLPTTKAGGEVETEPTGPLAVLKGFKDL 300
 LKG IFAKE+PY+A LP TKA G+VE EPTGPLAV KGFK+L
 Sbjct: 231 LKGAFLVAVLFLAFCLVITVIFAKEIPYKAIAPLP-TKANGQVEVEPTGPLAVFKGFKNL 289

Query: 301 PPGMPSVLLVTAITWLSWFFILYDTDWMGREIYHGD PKGSNAQISAFNEGVRVGAFLGL 360
 PPGMPSVLLVT +TWLSWFFILYDTDWMGREIYHGD PKG+ + +AF GVR GAFLGL
 Sbjct: 290 PPGMPSVLLVTGLTWLSWFFILYDTDWMGREIYHGD PKGTPDEANAFQAGVRAGAFGLL 349

Query: 361 LNSVILGFSSFLIEPMC RKVGRPVVWVTSNFMVCVMAATALISFWSLRDYG YVQDAIT 420
 LNSV+LGFSSFLIEP+C+++GPRVVWV+SNF+VC++MAA +IS+W+ +D HGY+Q AIT
 Sbjct: 350 LNSVILGFSSFLIEPLCKRLGPRVVWVSSNFLVCLSMACIISWWATQDMHGYIQHAIT 409

Query: 421 ANASIKAVCLVLFAFLGVPLAILYSVPFAVTAQLAATRGGGQGLCTGVLNISIVIPQVII 480
 A+ IK V L LFAFLGVPLAILYSVPFAVTAQLAA RGGGQGLCTGVLNI+IVIPQVII
 Sbjct: 410 ASKEIKIVSLALFAFLGVPLAILYSVPFAVTAQLAANRGGGQGLCTGVLNIAIVIPQVII 469

Query: 481 ALGAGPWDALFGKGNIPXXXXXXXXXXXXXXXXXXXXXPKISKRQFRAVSAGGH 533
 A+GAGPWD LFGKGNIP PKIS+RQFRAVS GGH
 Sbjct: 470 AVGAGPWDELFGKGNIPAFGMASAFALIGGIVGIFLLPKISRRQFRAVSGGGH 522

☐ >gi|19548165|gb|AAL90455.1|AF408845 1 sucrose transporter SUT1D [Triticum aestiv
 gi|20152875|gb|AAM13410.1|AF408844 1 sucrose transporter SUT1D [Triticum aestivum
 Length = 523

Score = 747 bits (1928), Expect = 0.0

Identities = 397/538 (73%), Positives = 432/538 (80%), Gaps = 20/538 (3%)

Query: 1 MARGDGGQLAELSAGVRGAAAVVDH-----VAPISLGRILLAGMVAPISLGRILLAGMVA 55
 MARG G ELS GV G ISLG RLILLAGMVA
 Sbjct: 1 MARGGGNGEVELSVGVGGGGGAAGGGEQPAVDISLG-----RLILLAGMVA 46

Query: 56 GGVQYGWALQLSLLTPYVQTLGLSHALTSFMWLCGPIAGLVVQPLVGLYSDRCTSRWGRR 115
 GGVQYGWALQLSLLTPYVQTLGLSHALTSFMWLCGPIAGLVVQP VGLYSD+CTSRWGRR
 Sbjct: 47 GGVQYGWALQLSLLTPYVQTLGLSHALTSFMWLCGPIAGLVVQPCVGLYSDKCTSRWGRR 106

Query: 116 RPFILTGCMILICVAVIVVGFSSDIGAALGDTKEHCSLYHGPRWHAAIVYVLGFWLLDFS 175
 RPFILTG+C+LIC+AV+VVGFS+DIGAALGD+KE CSLYHGPRWHAAIVYVLGFWLLDFS
 Sbjct: 107 RPFILTGILICIAVVVVGFSADIGAALGDSKEECSLYHGPRWHAAIVYVLGFWLLDFS 166

Query: 176 NTVQGPARAMMADLCDHHGPSAANSIFCSWMALGNILGYSSGSTNNWHKWFPFLKTSACC 235
 NTVQGPARA+MADL HGPSAANSIFCSWMALGNILGYSSGSTNNWHKWFPFL+T ACC
 Sbjct: 167 NTVQGPALMADLSAQHGPSAANSIFCSWMALGNILGYSSGSTNNWHKWFPFLRTRACC 226

Query: 236 EACANLKGXXXXXXXXXXXXXXXXXXXXXIFAKEVPYRANENLPTTKAGGEVETEPTGPLAVLK 295
 EACANLKG IFAKE+PY+A LP TKA G+VE EPTGPLAV K
 Sbjct: 227 EACANLKGAFVAVLFLAFCLVITVIFAKEIPYKAIAPLP-TKANGQVEVEPTGPLAVFK 285

Query: 296 GFKDLPPGMPSVLLVTAITWLSWFFILYD TDWMGREIYHGD PKGSNAQISAFNEGVRVG 355
 GFK+LPPGMPSVLLVT +TWLSWFFILYD TDWMGREIYHGD PKG+ +AF GVR G
 Sbjct: 286 GFKNLPPGMPSVLLVTGLTWLSWFFILYD TDWMGREIYHGD PKGTPEANAFQAGVRAG 345

Query: 356 AFGLLLNSVILGFSSFLIEPMCRKVGPRVWVTSNFMVCVAMAATALISFWSLRDYHGYV 415
 AFGLLLNSV+LGFSSFLIEP+C+++GPRVWVW+SNF+VC++MAA +IS+W+ +D HGY+
 Sbjct: 346 AFGLLLNSVILGFSSFLIEPLCKRLGPRVWVWSSNFLVCLSMACIISWATQDLHGYI 405

Query: 416 QDAITANASIKAVCLVLF AFLGVPLAILYSVPFAVTAQLAATRG GGGQGLCTGVLNISI VI 475
 Q AITA+ IK V L LFAFLG+PLAILYSVPFAVTAQLAA RGGGQGLCTGVLNI+IVI
 Sbjct: 406 QHAITASKEIKIVSLALFAFLGIPLAILYSVPFAVTAQLAAKRGGGQGLCTGVLNIAIVI 465

Query: 476 PQVIIALGAGPWDALFGKGNIPXXXXXXXXXXXXXXXXXXXXXPKISKRQFRAVSAGGH 533
 PQVIIA+GAGPWD LFGKGNIP PKIS+RQFRAVS GGH
 Sbjct: 466 PQVIIAVGAGPWDELFGKGNIPAFGMASAFALIGGIVGIFLLPKISRRQFRAVSGGGH 523

☐ >gi|16152148|gb|AAL14982.1|AF419298.1 sucrose transporter [Oryza sativa (indica
 Length = 506

Score = 586 bits (1511), Expect = e-166

Identities = 330/494 (66%), Positives = 375/494 (75%), Gaps = 11/494 (2%)

Query: 43 ISLGRILLAGMVAGGVQYGWALQLSLLTPYVQTLGLSHALTSFMWLCGPIAGLVVQPLVG 102
 ISL L LA MVAGGVQYGWALQLSLLTPY+QTLG+ HALTS MWLCGPIAGL+VQP VG
 Sbjct: 21 ISLSGLFLACMVAGGVQYGWALQLSLLTPYIQTGLIPHALTSVMWLCGPIAGLIVQPCVG 80

Query: 103 LYSDRCTSRWGRRRPFILTCMLICVAVIVVGFSSDIGAALGDTKEHCSLYHGPRWHA AI 162
 LYSD+CTS GRRRPFILTC++IC++VIV+GFSSDIG ALGD E C +Y GPR+HAA
 Sbjct: 81 LYSDKCTSSLGRRRPFILTCIIICISVIVIGFSSDIGYALGDATEDCKVYRGPRYHAAA 140

Query: 163 VYVLGFWLLDFSNNTVQGPARAMADLCHHGPSAANSIFCSWMALGNILGYSSGSTNNW 222
 ++LGFWLLDFSNNTVQGPARA+MADL HGPSAAN+IFCSWMALGNILGYSSGSTN+W
 Sbjct: 141 AFILGFWLLDFSNNTVQGPALMADLSGRHGPSAANAIFCSWMALGNILGYSSGSTNDW 200

Query: 223 HKWFPFLKTSACCEACANLKGXXXXXXXXXXXXXXXXXXXXXIFAKEVPYRANENLPTTKAGGE 282
 HKWFPFL T ACCEACANLK +FA+EV L A
 Sbjct: 201 HKWFPFLMTRACCEACANLKA AFLVAVVFLGLSTAVTMVFAREVA-----LDPVAAAKR 254

Query: 283 VETEPTGPLAVLKGFKDLPPGMPSVLLVTAITWLSWFFILYD TDWMGREIYHGD PKGSN 342
 E E +GPLAV KG K+LP GMPSVL+VT +TWLSWFFIL+DTDWMGREIYHG P GS
 Sbjct: 255 NEGEASGPLAVFKGMKNLPVGMPSVLIVTGLTWLSWFFILFD TDWMGREIYHGRPDGSP 314

Query: 343 AQISAFNEGVRVGAFGLLLNSVILGFSSFLIEPMCRKVGPRVWVTSNFMVCVAMAATAL 402
 A+++AF EGVR GAFGLLLNS++LG SSFLIEPMCR++G R VWV S+ +VCVAMAA ++
 Sbjct: 315 AEVTAFAQEGVRQGAFLGLLLNSIVLGISSFLIEPMCRRLGARAVWVMSSAVVCVAMAAVSV 374

Query: 403 ISFWSLRDYHGYVQDAITANAS---IKAVCLVLF AFLGVPLAILYSVPFAVTAQLAATRG 459
 +S WSL D+ G VQDA A A ++A L LF FLG+P A+L SVPFAVTAQL A+RG
 Sbjct: 375 LSAWSLGD FGGSVQDAARAPAEEGVRASALALFVFLGLPFAVLCSVPFAVTAQLTASRG 434

Query: 460 GGQGLCTGVLNISI VIPQVIIALGAGPWDALFGKGNIPXXXXXXXXXXXXXXXXXXXXXPK 519
 GGQGLCTGVLNISI V+PQ+ IALGAGPWD LFG+GNIP PK
 Sbjct: 435 GGQGLCTGVLNISI VVPQMAIALGAGPWDELFGEGNIPAFAMASVFAAAAAAGVVLLPK 494

Query: 520 ISKRQFRAVSAGGH 533
 +S R AGGH
 Sbjct: 495 VSVRSVSM--AGGH 506

☐ >gi|15718401|dbj|BAB68368.1| sucrose transporter [Oryza sativa (japonica cultiva
 Length = 506

Score = 586 bits (1511), Expect = e-166

Identities = 332/494 (67%), Positives = 376/494 (76%), Gaps = 11/494 (2%)

Query: 43 ISLGRILLAGMVAGGVQYGWALQLSLLTPYVQTLGLSHALTSMWLCGPIAGLVVQPLVG 102
 ISL L LA MVAGGVQYGWALQLSLLTPYVQTLG+ HALTS MWLCGPIAGL+VQP VG
 Sbjct: 21 ISLSGLFLACMVAGGVQYGWALQLSLLTPYVQTLGIPHALTSVMWLCGPIAGLIVQPCVG 80

Query: 103 LYSDRCTSRWGRRRPFILTCMLICVAVIVVGFSSDIGAALGDTKEHCSLYHGPRWHA 162
 LYSD+CTS GRRRPFILTC++IC++VIV+GFSSDIG ALGDT E C +Y GPR+HAA
 Sbjct: 81 LYSDKCTSSLGRRRPFILTCIIICISVIVIGFSSDIGYALGDTTDEDCKVYRGPRYHAAA 140

Query: 163 VYVLGFWLLDFSNNTVQGPARAMMADLCDHHGPSAANSIFCSWMALGNILGYSSGSTNNW 222
 ++LGFWLLDFSNNTVQGPARG+MADL HGPSAAN+IFCSWMALGNILGYSSGSTN+W
 Sbjct: 141 AFILGFWLLDFSNNTVQGPARGMADLSGRHGPSAANAIFCSWMALGNILGYSSGSTNDW 200

Query: 223 HKWFPFLKTSACCEACANLKGXXXXXXXXXXXXXXXXXXXXIFAKEVPYRANENLPTTKAGGE 282
 HKWFPFL T ACCEACANLK +FA+EV L A
 Sbjct: 201 HKWFPFLMTRACCEACANLKAFLVAVVFLGLSTAVTMVFAREVA-----LDPVAAAKR 254

Query: 283 VETEPTGPLAVLKGFKDLPPGMPSVLLVTAITWLSWFPFIFYDWDWMGREIYHGDPKGSN 342
 E E +G LAV KG K+LP GMPSVL+VT +TWLSWFPFIL+DTDWMGREIYHG P GS
 Sbjct: 255 NEGEASGLLAVFKGMKNLPVGMPSVLIVTGLTWLSWFPFILFDTDWMGREIYHGRPDGSP 314

Query: 343 AQISAFNEGVRVGAFLLLNSVILGFSSFLIEPMCCKVGPVVVWVTSNFMVCVAMAATAL 402
 A+++AF EGVR GAFGLLLNS++LG SSFLIEPMC++G R VWV S+ +VCVAMAA ++
 Sbjct: 315 AEVTAFAQEGVRQGAFLLLNSIVLGISSFLIEPMCRRLGARAVVWMSSAVVCVMAAAVSV 374

Query: 403 ISFWSLRDYGHYVQDAITANAS---IKAVCLVLFAFLGVPLAILYSVPFAVTAQLAATRG 459
 +S WSL D+ G VQDA A A ++A L LF FLG+P A+L SVPFAVTAQLAA+RG
 Sbjct: 375 LSAWSLGDGFGSVQDAARAPAEEGVRSALALFVFLGLPFAVLCSVPFAVTAQLAASRG 434

Query: 460 GGQGLCTGVLNIVIPQVIALGAGPWDALFGKGNIPXXXXXXXXXXXXXXXXXXXXPK 519
 GGQGLCTGVLNIVIPQ+ IALGAGPWD LFG+GNIP PK
 Sbjct: 435 GGQGLCTGVLNIVIPQMAIALGAGPWDELFGEGNIPAFAMASVFAAAAAAGVVLTPK 494

Query: 520 ISKRQFRAVSAGGH 533
 +S R AGGH
 Sbjct: 495 VSVRSVSM--AGGH 506

☐ >gi|21063927|gb|AAM29153.1| sucrose transporter 2 [Citrus sinensis]
 Length = 607

Score = 526 bits (1356), Expect = e-148
 Identities = 286/559 (51%), Positives = 359/559 (64%), Gaps = 54/559 (9%)

Query: 27 APISLGRILLAGMVAPISLGRILLAGMVAGGVQYGWALQLSLLTPYVQTLGLSHALTSM 86
 +PI G A SL L+L+ VA GVQ+GWALQLSLLTPY+QTLG+ HA +SF+
 Sbjct: 49 SPIPNGTSNFAVRPKQCSLITLVLSTVAAGVQFGWALQLSLLTPYIQTGLIQHAFSSFI 108

Query: 87 WLCGPIAGLVVQPLVGLYSDRCTSRWGRRRPFILTCMLICVAVIVVGFSSDIGAALGDT 146
 WLCGPI GLVVQP VG++SD+CTS++GRRRPFIL GC++I VAVI++GFS+DIG LGDT
 Sbjct: 109 WLCGPITGLVVQPCVGIWSDKCTSKYGRRRPFILAGCLMISVAVIIIGFSADIGYILGDT 168

Query: 147 KEHCSLYHGPRWHAIVYVLGFWLLDFSNNTVQGPARAMMADLCDHHGPSAANSIFCSWM 206
 KEHCS + G R AA V+V+GFWLLD +NNTVQGPARG++ADL ++AN+I CSWM
 Sbjct: 169 KEHCSKFRGTRTRAAFFVFIGFWLLDLNNTVQGPARGALLADLSGPDQRNSANAILCSWM 228

Query: 207 ALGNILGYSSGSTNNWHKWFPFLKTSACCEACANLKGXXXXXXXXXXXXXXXXXXXXIFAKEV 266
 A+GNILG+S+G++ +WH+WFPFL + ACC AC NLK FA EV
 Sbjct: 229 AVGNILGFSAGASGSWHRWFPLTSRACCAACGNLKAFLVAVVFLTLCALVTIYFADEV 288

Query: 267 PYRANE-----NLPT--TKAGGEVET----- 285
 P N+ ++P G +VE+
 Sbjct: 289 PLTVNQPNHLTDSAPLLDDPQRTAISKSKHDMPAAPNANGNKVESGHERDANLKHISKKA 348

Query: 286 -EPT-----GPLAV----LKGFKDLPPGMPSVLLVTAITWLSWFPFIFYDWDWMGREIYH 335
 +P GP AV L + LPP M VL+V A+TWLSWFPF L+DTDWMGRE+YH
 Sbjct: 349 EDPNGSFNDGPGAVLVNLLTSLRHLPPAMHVVLVVMALTWLSWFPFIFYDWDWMGREVYH 408

Query: 336 GDPKGSNAQISAFNEGVRVGAFGLLLNSVILGFSSFLIEPMCRKVGPRVVWVTSNFMVCV 395
 GDPKG++ ++ +++GVR GAFGLLLNSV+LG SSFLIEPMCR +G R+VW SNF+V
 Sbjct: 409 GDPKGNDEHKFYDQGVREGAFGLLLNSVVLGVSSFLIEPMCRWIGSRLVWAI SNFVFA 468

Query: 396 AMAATALISFWSL-RDYHGYVQDAITANASIKAVCLVLF AFLGVPLAILYSVPFAVTAQL 454
 MA TA+IS S+ R+ ++ I AN +IK LV+F LG PLAI YSVPFA+T +L
 Sbjct: 469 CMATTAIISVISVRRNILEGIEHGIGANQAIVASLVVFTLLGFPLAITYSVPFAITGEL 528

Query: 455 AATRGGGQGLCTGVLNISIVIPQVIALGAGPWDALFGKGNIPXXXXXXXXXXXXXXXXXXXX 514
 A GGGQGL GVLN++IVIPQ+I++LGAGPWDALFG GNIP
 Sbjct: 529 TADSGGGQGLAIGVLNLAIVIPQMIVSLGAGPWDALFGGGNIPAFGLASLSALAGGVVAT 588

Query: 515 XXXPKISKRQFRAVSAGGH 533
 P +S F S+G H
 Sbjct: 589 LKLPHLSSNSF--TSSGFH 605

☐ >gi|29467454|dbj|BAC67164.1| sucrose transporter [Oryza sativa (japonica cultivata)]
 Length = 595

Score = 526 bits (1355), Expect = e-148
 Identities = 267/499 (53%), Positives = 344/499 (68%), Gaps = 48/499 (9%)

Query: 47 RLILAGMVAGGVQYGWALQLSLLTPYVQTLGLSHALTSFMWLCGPIAGLVVQPLVGLYSD 106
 +L+LA MVA GVQ+GWALQLSLLTPY+QTLG+ HA+ SF+WLCGPI G VVQP VG++SD
 Sbjct: 61 KLVLACMVAAGVQFGWALQLSLLTPYIQTLGIDHAMASFIWLCGPITGFVVQPCVGVWSD 120

Query: 107 RCTSRWGRRRPFILTGCMCLICVAVIVVGFSSDIGAALGDTKEHCSLYHGPRWHAAIVYVL 166
 +C S++GRRRPFIL GC++IC AV ++GFS+D+G LGDT EHCS Y G R+ AAI++VL
 Sbjct: 121 KCRSKYGRRRPFILAGCLMICFAVTLIGFSADLGYILGDTTEHCSTYKGSRFRAAIIIFVL 180

Query: 167 GFWLLDFSNNTVQGPARAMMADLCDHHGPSAANSIFCSWMALGNILGYSSGSTNNWHKWF 226
 GFW+LD +N+TVQGPARA++ADL ++AN+IFC+WMA+GN+LG+SSG++ NWHKWF
 Sbjct: 181 GFWMLDLANHTVQGPARALLADLSGPDQCNSANAIFCTWMAVGNVLGFSSGASGNWHKWF 240

Query: 227 PFLKTSACCEACANLKGXXXXXXXXXXXXXXXXXXXXIFAKEVPYR----- 269
 PFL T ACCEAC+NLK FA+E+P
 Sbjct: 241 PFLMTRACCEACSNLKAFLVAVVFLFCMSVTLYFAEEIPLPTDAQRLSDSAPLLNGS 300

Query: 270 -----ANENLPTTKAGGE-VETEPTGPLAV----LKGFK 298
 AN N + + E VE GP AV L +
 Sbjct: 301 RDDNNASNEPRNGALPNGHTDGSNVPANSNAEDSNSNRENVEVFNDGPGAVLVNILTSMR 360

Query: 299 DLPPGMPSVLLVTAITWLSWFPFILIYDTDWMGREIYHGD PKGSNAQISAFNEGVRVGAFG 358
 LPPGM SVLLV A+TWLSWFPF L+DTDWMGRE+YHGD G+ ++ A++ GVR GAFG
 Sbjct: 361 HLPPGMYSVLLVMALTWLSWFPFLLFDTDWMGREVYHGD PNGNLSEKAYDNGVREGAFG 420

Query: 359 LLLNSVILGFSSFLIEPMCRKVGPRVVWVTSNFMVCVAMAATALISFWSLRDYHGYVQDA 418
 LLLNSV+LGF SFL++P+CR +G R+VW SNF V + M ATA++S+ S Y +
 Sbjct: 421 LLLNSVVLGFSGFLVDPLCRLMGARLVWAI SNFTVFICMLATAILSWISFDLYSSKLHHI 480

Query: 419 ITANASIKAVCLVLF AFLGVPLAILYSVPFAVTAQLAATRGGGQGLCTGVLNISIVIPQV 478
 I AN ++K L++F+ LG+PL+I Y VPF+VTA+L A G GQGL TGVLN++IV+PQ+
 Sbjct: 481 IGANKTVKNSALIVFSLGLPLSITYGVPF SVTAELTAGTSGQGLATGVLNLAIVVPQI 540

Query: 479 IIALGAGPWDALFGKGNIP 497
 +++LGAGPWDALFG GN+P
 Sbjct: 541 VVSLGAGPWDALFGGGNVP 559

☐ >gi|10119908|gb|AAG12987.1|AF166498.1 sucrose transporter-like protein [Lycopersicon
 Length = 604]

Score = 525 bits (1353), Expect = e-148
 Identities = 269/508 (52%), Positives = 336/508 (66%), Gaps = 54/508 (10%)

Query: 44 SLGRLLILAGMVAGGVQYGWALQLSLLTPYVQTLGLSHALTSFMWLCGPIAGLVVQPLVGL 103
SL LIL+ VA GVQ+GWALQLSLLTPY+QTLG+ HA +SF+WLCGPI GLVVQP VG+

Sbjct: 62 SLLTLILSCTVAAGVQFGWALQLSLLTPYIQTGLGIEHAFSSFIWLCGPITGLVVQPCVGI 121

Query: 104 YSDRCTSRWGRRRPFILTGCMCLICVAVIVVGFSSDIGAALGDTKEHCSLYHGPRWHAAIV 163
+SD+C S++GRRRPFI G ++I +AVI++GFS+DIG LGDTKEHCS + G R AAIV

Sbjct: 122 WSDKCHSKYGRRRPFIFIGAVMISIAVIIIGFSADIGYLLGDTKEHCSTFKGTRSRAAIV 181

Query: 164 YVLGFWLLDFSNNTVQGPARAMMADLCDHHGPSAANSIFCSWMALGNILGYSSGSTNNWH 223
+V+GFW+LD +NNTVQGPARGA++ADL + AN++FCSWMA+GNILG+S+G++ WH

Sbjct: 182 FVVGFWMLDLANNTVQGPARGALLADLSGPDQRNTANAVFCSWMAVGNILGFSAGASGGWH 241

Query: 224 KWFPFLKTSACCEACANLKGXXXXXXXXXXXXXXXXXXXXXIFAKEVP----- 267
+WFPFL ACCE C NLK FA EVP

Sbjct: 242 RWFPFLTNACCEPCGNLKAFLVAVVFLTLCTLVTLTYFANEVPLSPKQYKRMSDSAPLL 301

Query: 268 -----YRAN-----ENLPTTKAGGEVETEPTGP 290
YR + E P G P

Sbjct: 302 DSPQNTGFDLSQSKRELQYRNSVANNESEMGHVADNSPKNEEQRPDKDQGDSFADSPGAV 361

Query: 291 LA-VLKGFKDLPPGMPSVLLVTAITWLSWFPFIFYDTDWMGREIYHGD PKGSNAQISAFN 349
L +L + LPP M SVL+V A+TWLSWFPF L+DTDWMGRE+YHGD PKG +++A+N

Sbjct: 362 LVNLLTSLRHLPPAMHSVLIVMALTWLSWFPFFLFDTDWMGREVYHGD PKGEADEVNAYN 421

Query: 350 EGV RVGAFGLLLNSVILGFSSFLIEPMC RKVGPVVVTSNFMVCVAMAATALISFWSLR 409
+GVR GAFGLLLNSV+LG SSFLIEPMC+ +G R+VW SNF+V V MA TA+IS S+

Sbjct: 422 QGVREGAFGLLLNSVVLGVSSFLIEPMC KWIGSRLVWAVSNFIVFVCMATAIISVVSIS 481

Query: 410 DYHGYVQDAITANASIKAVCLVLFAFLGVPLAILYSVPFAVTAQLAATRGGGQGLCTGVL 469
VQ I A S + LV+F+ LG+PLA+ YSVPF++TA+L A GGGQGL GVL

Sbjct: 482 ANTQGVQHVIGATRSTQIAALVVFSLGLIPLAVTYSVPFSITAELTADAGGGQGLAIGVL 541

Query: 470 NISIVIPQVIIALGAGPWDALFGKGNIP 497
N++IV+PQ+++LGAGPWDALFG GNIP

Sbjct: 542 NLAIVVPQMVSLLGAGPWDALFGGKNIP 569

☐ >gi|15227049|ref|NP_178389.1| putative sucrose/H⁺ symporter; protein id: At2g028
thaliana]

gi|25344715|pir|G84441 probable sucrose-proton symporter [imported] - Arabidopsi
gi|3461813|gb|AAC32907.1| putative sucrose/H⁺ symporter [Arabidopsis thaliana]
gi|8052190|emb|CAB92307.1| sucrose transporter [Arabidopsis thaliana]
Length = 594

Score = 523 bits (1348), Expect = e-147

Identities = 261/501 (52%), Positives = 336/501 (67%), Gaps = 47/501 (9%)

Query: 44 SLGRLLILAGMVAGGVQYGWALQLSLLTPYVQTLGLSHALTSFMWLCGPIAGLVVQPLVGL 103
SL L+L+ VA GVQ+GWALQLSLLTPY+QTLG+SHA +SF+WLCGPI GLVVQP VG+

Sbjct: 59 SLVTLVLSCTVAAGVQFGWALQLSLLTPYIQTGLGISHAFSSFIWLCGPITGLVVQPFVGI 118

Query: 104 YSDRCTSRWGRRRPFILTGCMCLICVAVIVVGFSSDIGAALGDTKEHCSLYHGPRWHAAIV 163
+SD+CTS++GRRRPFI G +I +AVI++GFS+DIG LGD+KEHCS + G R AA+V

Sbjct: 119 WSDKCTSKYGRRRPFILVGSFMISIAVIIIGFSADIGYLLGDSKEHCSTFKGTRTRAADV 178

Query: 164 YVLGFWLLDFSNNTVQGPARAMMADLCDHHGPSAANSIFCSWMALGNILGYSSGSTNNWH 223
+++GFWLLD +NNTVQGPARGA++ADL + AN++FC WMA+GNILG+S+G++ W

Sbjct: 179 FIIGFWLLDLANNTVQGPARGALLADLSGPDQRNTANAVFCLWMAIGNILGFSAGASGKWQ 238

Query: 224 KWFPFLKTSACCEACANLKGXXXXXXXXXXXXXXXXXXXXXIFAKEVPYRAN----- 271
+WFPFL + ACC AC NLK FAKE+P+ +N

Sbjct: 239 EWFPFLTSRACCAACGNLKAFLVAVVFLTICTLVTIYFAKEIPFTSNKPTRIQDSAPLL 298

Query: 272 -----ENLPTTKAGGEVETEPTGPLAV-----LKG 296
E ++ + ET GP +V L

Sbjct: 299 DDLQSKGLEHSLNNGTANGIKYERVERDTEQFGNSENEHQDETYVDGPGSVLVNLLTS 358

Query: 297 FKDLPPGMPSVLLVTAITWLSWFPFIFYD TDWMGREIYHGDPKGSNAQISAFNEGVRVGA 356
 + LPP M SVL+V A+TWLSWFPF L+DTDWMGRE+YHGDP G + + +++GVR GA
 Sbjct: 359 LRHLPPAMHSVLIVMALTWLSWFPFFLFD TDWMGREVYHGDP TGD SLHME LYDQGVREGA 418

Query: 357 FGLLLNSVILGFSSFLIEPMC RKVGP RVVWVTSNFMVCVAMAATALISFWSLRDYHGYVQ 416
 GLLLSNV+LG SSFLIEPMC+++G RVVW SNF V MA TA+IS SL D ++
 Sbjct: 419 LGLLLNSVVLGISSFLIEPMCQRMGARVVWALS NF TVFACMAGTAVISLMSLSDDKNGIE 478

Query: 417 DAITANASIKAVCLVLF AFLGVPLAILYSVPFAVTAQLAATRGGGQGLCTGVNLISIVIP 476
 + N + + +++FA LG PLAI YSVPF+VTA++ A GGGQGL GVLN++IVIP
 Sbjct: 479 YIMRGNETTRTAAVIVFALLGFPLAITYSVPFSVTA EVTADSGGGQGLAIGVLNLAIVIP 538

Query: 477 QVIALGAGPWDALFGKGNIP 497
 Q+I++LGAGPWD LFG GN+P
 Sbjct: 539 QMIVSLGAGPWDQLFGGKNLP 559

☐ >gi|6434831|gb|AAF08330.1|AF021809.1 putative sucrose transporter [Vitis vinifera]
 Length = 612

Score = 517 bits (1331), Expect = e-145
 Identities = 272/507 (53%), Positives = 340/507 (67%), Gaps = 54/507 (10%)

Query: 45 LGRILLAGMVAGGVQYGWALQLSLLTPYVQTLGLSHALTSFMWLCGPIAGLVVQPLVGLY 104
 L LIL+ M+A GVQ+GWALQLSLLTPY+QTLG+ HA +SF+WLCGPI GLVVQP VG++
 Sbjct: 63 LRTLILSCMIAAGVQFGWALQLSLLTPYIQTLGIEHAFSSFIWLCGPITGLVVQPCVGIW 122

Query: 105 SDRCTSRWGRRRPFILTGCM LICVAVIVGFSSDIGAALGDTKEHCSLYHGPRWHAAIVY 164
 SD+C+S++GRRRPFIL G ++I VAV ++GFS+DIG LGDT C + G R AAI++
 Sbjct: 123 SDKCSSKYGRRRPFILAGSLMISVAVTIIGFSADIGYLLGDTNMDCRKFKGTRTWAAIIF 182

Query: 165 VLGFWLLDFSNN TVQGPARAMADLCDHHGPSAANSIFCSWMALGNILGYSSGSTNNWHK 224
 VLGFW+LD +NNTVQGPARA++ADL ++AN+IFCSWMA+GNILG+S+G++ +WH+
 Sbjct: 183 VLGFWMLDLANN TVQGPARALLADLSGPDQRNSANAIFCSWMAVGNILGFSAGASGHWHR 242

Query: 225 WFPFLKTSACCEACANLKGXXXXXXXXXXXXXXXXXIFAKEVP----- 267
 WFPFL ACCEAC NLK FA+EVP
 Sbjct: 243 WFPFLNLKACCEACGNLKAFLIAVFLTLCTLVTLTYFAEEVPLMAYQPHHLSDSAPLLD 302

Query: 268 -----YRANENLP--TTKAGGEVETEPTGPLAV-- 293
 Y N+N T + E+ GP AV
 Sbjct: 303 NPQQIGFDNSKSKLDMSAVDNATGNNPESSYEINKNAKHLTPIVQE QNESFSDGPGAVLV 362

Query: 294 --LKGFKDLPPGMPSVLLVTAITWLSWFPFIFYD TDWMGREIYHGDPKGSNAQISAFNEG 351
 L + LPP M SVLLV A++WLSWFPF L+DTDWMGRE+YHGDPKG + + A++ G
 Sbjct: 363 NLLTSLRHLPPAMHSVLLVMALSWSWFPFFLFD TDWMGREVYHGDPKGDES AVKAYDAG 422

Query: 352 VRVGA FGLLLNSVILGFSSFLIEPMC RKVGP RVVWVTSNFMVCVAMAATALISFWSLRDY 411
 VR GAFGLLLNSV LG SSFLIEPMC+++G R+VW SNF+V MA TA+IS S+ +Y
 Sbjct: 423 VREGAFGLLLNSVDLGISSFLIEPMCQRMGARLVWAMSNFIVFACMAGTAIISLVS VNEY 482

Query: 412 HGY-VQDAITANASIKAVCLVLF AFLGVPLAILYSVPFAVTAQLAATRGGGQGLCTGVNL 470
 +Q AI N +IK LV+FA LG PL+I YSVPF++TA+L A GGGQGL GVLN
 Sbjct: 483 ITEGIQHAIGENRAIKIASLVVFALLGFPLSITYSVPFSITAE LTADTGGGQGLAIGVLN 542

Query: 471 ISIVIPQVIALGAGPWDALFGKGNIP 497
 ++IVIPQ+I++LGAGPWDALFG GNIP
 Sbjct: 543 LAIVIPQMIVSLGAGPWDALFGGKNIP 569

☐ >gi|29467456|dbj|BAC67165.1| sucrose transporter [Oryza sativa (japonica cultivar)]
 Length = 535

Score = 502 bits (1293), Expect = e-141
 Identities = 261/489 (53%), Positives = 333/489 (68%), Gaps = 8/489 (1%)



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RPS-BLAST 2.2.5 [Nov-16-2002]

Query= local sequence:
(533 letters)Database: cdd.v1.61
10,927 PSSMs; 2,688,589 total columns

Click on boxes for multiple alignments

[Show](#) Domain RelativesPSSMs producing significant alignments: Score E
(bits) value[gnl|CDD|11918](#) COG2211, MelB, Na⁺/melibiose symporter and related transporter... 47.9 3e-06

[gnl|CDD|11918](#), COG2211, MelB, Na⁺/melibiose symporter and related transporters [Carbohydrate transport and metabolism]CD-Length = 467 residues, only 26.3% aligned
Score = 47.9 bits (114), Expect = 3e-06

Query:	42	PISLGRILLAGM--VAGGVQYGWALQLSLTPYVQTLGLSHALTSFMWLCGPIAGLVVQP	99
Sbjct:	8	KLSLKEKIGYGLGDFASNFAFG-IVVLYLLFFYTDVFGLSAALAGTIFLVARIIDAITDP	66
Query:	100	LVGLYSRDRCTSRWGRRRPFILTGCM LICVAVIVVGFSSDIGAALGDTKEHCSLYHGPRWH	159
Sbjct:	67	IMGFIVDRTRSRWGRFRPWLLWGAIPFAIVAVLLFITPDFS-----MTGKLIY	114
Query:	160	AAIVYVLGFWLLDFSN	175
Sbjct:	115	ALVTYMLLGLGYTLVN	130

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RPS-BLAST 2.2.5 [Nov-16-2002]

Query= local sequence:
(533 letters)

Database: cdd.v1.61
10,927 PSSMs; 2,688,589 total columns

Click on boxes for multiple alignments



[Show](#) Domain Relatives

PSSMs producing significant alignments: Score E
(bits) value

[gnl|CDD|11918](#) COG2211, MelB, Na⁺/melibiose symporter and related transporter... 47.9 3e-06

[gnl|CDD|11918](#), COG2211, MelB, Na⁺/melibiose symporter and related transporters [Carbohydrate transport and metabolism]

CD-Length = 467 residues, only 26.3% aligned
Score = 47.9 bits (114), Expect = 3e-06

Query: 42	PISLGRILLAGM--VAGGVQYGWALQLSLTPYVQTLGLSHALTSFMWLCGPIAGLVVQP	99
Sbjct: 8	KLSLKEKIGYGLGDFASNFAFG-IVVLYLLFFYTDVFGLSAALAGTIFLVARIIDAITDP	66
Query: 100	LVGLYSDRCTSRWGRRRPFILTGCMLICVAVIVVGFSSDIGAALGDTKEHCSLYHGPRWH	159
Sbjct: 67	IMGFIVDRTRSRWGRFRPWLLWGAIPFAIVAVLLFITPDFS-----MTGKLIY	114
Query: 160	AAIVYVLGFWLLDFSN	175
Sbjct: 115	ALVTYMLLGLGYTLVN	130

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PubMed	Nucleotide	Protein	Genome	Structure	PMC	Taxonomy	OMIM	Books
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		Limits	Preview/Index	History	Clipboard		Details	
Display	default	▼ Show: 20	▼ Send to	File	▼ Get Subsequence			

☐ 1: AAF90181. sucrose transport...[gi:9624451]

[BLink](#), [Domains](#), [Links](#)



LOCUS AAF90181 538 aa linear PLN 07-APR-2003
 DEFINITION sucrose transporter [Oryza sativa (indica cultivar-group)].
 ACCESSION AAF90181
 VERSION AAF90181.1 GI:9624451
 DBSOURCE accession AF280050.1
 KEYWORDS
 SOURCE Oryza sativa (indica cultivar-group)
 ORGANISM Oryza sativa (indica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.
 REFERENCE 1 (residues 1 to 538)
 AUTHORS Aoki,N., Hirose,T., Scofield,G.N., Whitfeld,P.R. and Furbank,R.T.
 TITLE The sucrose transporter gene family in rice
 JOURNAL Plant Cell Physiol. 44 (3), 223-232 (2003)
 MEDLINE 22555500
 PUBMED 12668768
 REFERENCE 2 (residues 1 to 538)
 AUTHORS Whitfeld,P.R. and Furbank,R.T.
 TITLE Direct Submission
 JOURNAL Submitted (19-JUN-2000) CSIRO Plant Industry, GPO Box 1600,
 Canberra, ACT 2601, Australia
 COMMENT Method: conceptual translation supplied by author.
 FEATURES
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 /cultivar="IR36"
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 CDS 1..538
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 AF280050.1:5208..5241,AF280050.1:5408..5507,
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ORIGIN

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181 ntvqgparal madlsgrhgp gtansifcsw mamgnilgys sgstnnwhkw fpflktracc
241 eacanlkgaf lvavifslc lvitlifake vpfkgnaalp tksnepaepe gtgplavlkq
301 frnlptgmps vlivtgltwl swfpfilydt dwmgreiyhg dpkgtdpqie afnqgvraga
361 fglllnsivl gfssflipep crkvgprvvw vtsnflvcia maatalisfw slkdfhgtvq
421 kaitadksik avclvlfafl gvplavlysv pfavtaqlaa trgggggglct gvlnisivip
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Search	Protein	▼	for					Go	Clear
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☐ 1: AAF90181. sucrose transport...[gi:9624451][BLink](#), [Domains](#), [Links](#)

LOCUS AAF90181 538 aa linear PLN 07-APR-2003
DEFINITION sucrose transporter [Oryza sativa (indica cultivar-group)].
ACCESSION AAF90181
VERSION AAF90181.1 GI:9624451
DBSOURCE accession AF280050.1
KEYWORDS
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (residues 1 to 538)
AUTHORS Aoki,N., Hirose,T., Scofield,G.N., Whitfeld,P.R. and Furbank,R.T.
TITLE The sucrose transporter gene family in rice
JOURNAL Plant Cell Physiol. 44 (3), 223-232 (2003)
MEDLINE 22555500
PUBMED 12668768
REFERENCE 2 (residues 1 to 538)
AUTHORS Whitfeld,P.R. and Furbank,R.T.
TITLE Direct Submission
JOURNAL Submitted (19-JUN-2000) CSIRO Plant Industry, GPO Box 1600,
Canberra, ACT 2601, Australia
COMMENT Method: conceptual translation supplied by author.
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AF280050.1:4321..4386,AF280050.1:4719..4817,
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AF280050.1:5208..5241,AF280050.1:5408..5507,
AF280050.1:5674..5749,AF280050.1:5975..6169,
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ORIGIN

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421 kaitadksik avclvlfafl gvplavlysv pfavtaqlaa trggggglct gvlnisivip
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☐ 1: BAA83501. Sucrose Transport...[gi:5771354]

[BLink](#), [Domains](#), [Links](#)

LOCUS BAA83501 521 aa linear PLN 26-AUG-1999
 DEFINITION Sucrose Transporter [Zea mays].
 ACCESSION BAA83501
 VERSION BAA83501.1 GI:5771354
 DBSOURCE accession [AB008464.1](#)
 KEYWORDS .
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 REFERENCE 1 (sites)
 AUTHORS Aoki,N., Hirose,T., Takahashi,S., Ono,K., Ishimaru,K. and Ohsugi,R.
 TITLE Molecular cloning and expression analysis of a gene for a sucrose
 transporter in maize (Zea mays L.)
 JOURNAL Plant Cell Physiol. (1999) In press
 REFERENCE 2 (residues 1 to 521)
 AUTHORS Aoki,N.
 TITLE Direct Submission
 JOURNAL Submitted (24-OCT-1997) Naohiro Aoki, Japan International Research
 Center for Agricultural Sciences, Biological Resources Division;
 1-2 Ohwashi, Tsukuba, Ibaraki 305, Japan
 (E-mail:naoki@ss.jircas.affrc.go.jp, Tel:81-0298-38-6305,
 Fax:81-0298-38-6650)
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 /db_xref="taxon:4577"
 Protein 1..521
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ORIGIN

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181 hhgpsaansi  fcswmalgni  lgyssgstnn  whkwfpfllt  nacceacanl  kgaflvavvf
241 lvmcltvtlf  fanevpyrgn  qnlptkange  vetepsgpla  vlkgfknlp  gmpsvllvtg
301 ltwlswfpfi  lytdwmgre  iyhgdpkgsn  aqisafdegv  rvgsfgllln  sivlgfssfl
361 iepmcrkvqp  rvvwtsnfm  vcvamaatal  isfwslkdyh  gyvqdaitas  tsikavclvl
421 faflgvplai  lysvpfavta  qlaatkgggg  glctgvlnis  ivipqviial  gagpwdalfg
481 kgnipafgva  sgfaliggyv  gvflpkisk  rqrfravsagg  h

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